MASS SPECTRAL METHODS FOR THE ANALYSIS OF ORGANIC RESIDUES IN MEAT

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Mass Spectrometry has evolved in recent years through the development of lower cost, more dependable and computer controlled systems, to instruments which can provide rapid and routine analysis in a wide range of areas. The objectives of this lecture will be to provide a simple understanding of mass spectral techniques and their combination with chromatographic methods and to show the advantages and uniqueness of this approcach for the analysis of organic residues in meat. In addition, the potential of such systems, through incorporation of a high level of automation, for rapid analysis to ensure meat quality will be discussed.

BASICS

A mass spectrometer can be divided into four key features:

i) Sample introduction system

ii) Ion source

iii) Mass analyser

iv) Detector

and it is important to remember that the system works under vacuum.

The sample introduction systems which are relevant in our context are:

The direct insertion probe where sample is loaded into a crucible or onto a wire, inserted into the ion source and by heating, the sample is vaporized. Alternatively, sample can be introduced via a gas chromatograph or a high-performance liquid chromatograph. All these systems can be automated.

Sample is ionized in the ion source and a variety of ionization techniques exist which can be divided into those which ionize sample in the vapour phase or in the condensed phase. In the former case, compounds which have volatility and are reasonably thermally stable can be studied, whilst the other forms of ionization are used for involatile and highly polar compounds. For ionization in the vapour phase electron impact (EI) or chemical ionization (CI) are usually used. To effect EI high energy electrons are used, whilst for CI a gas is ionized and these ions are used to ionize the sample. Fast atom bombardment and thermospray ionization are the most widely used methods for ionization from the condensed phase.

Ions generated are subsequently separated in terms of their mass/charge (m/z) ratio in the mass analyser. The charge i usually 1 and hence in general terms ions are separated according to their mass. Mass analysers are usually either quadrupoles or a combination of magnetic and electric fields.

Detection of the ions is effected using a photomultiplier and normally a computer is used to process data and control many instrumental parameters.

The information available from the mass spectrum produced varies according to the ionization method used. A major utility of the technique is that spectra can be obtained from very small sample amounts (10^{-9} g) and if full spectra are not required, even lower amounts (10^{-12} g) of compound can be detected. In the case of EI, the spectrum is a finger print of the compound and computer library searches can be used to provide positive identification if the compound is known. If an unknown compound is being studied the various spectra can provide considerable structural information.

Overall, a mass spectrometer can provide specific identification on very small amounts of sample and use of appropriate ionization methods can provide selective ionization for particular classes of compound. Combination of the mass spectrometer with a chromatograph adds further dimensions, since complex mixtures can be separated on the chromatograph and spectra obtained from the individual components. Tandem mass spectrometers, which have more mass analyser sections and enable reactions to be performed in the analyser region of the instrument provide increased specificity of identification and enable sample work-up procedures to be considerably reduced.

Analysis of organic residues in meat presents a challenge to the analytical chemist since legislation increasingly requires that very small amounts of compound are specifically identified. Hence, one is often looking for between 1 part in a million or a few parts per billion of specific compounds in a complex matrix of other compounds. The classes of compound requiring location can vary widely in structural types and include antibiotics, antihelmintics, hormones, β-agnonists, organochlorines, thyreostatics and mycotoxins. Techniques such as chromatography and radioimmunoassay are often used for such types of analysis. However, both can lack specificity of identification and in the case of gas chromatography extensive sample pretreatment is usually required.

Using examples of studies e.g. on antibiotics and hormones, the utility of mass spectrometric techniqes and combined chromatographic/mass spectrometric techniques for the rapid analysis of these residues in meat will be discussed. Particular attention will be paid to reduction in sample work-up time and speed of analysis. In addition, the potential of automated sample introduction techniques together with mass spectrometry for the rapid analysis of meat will be explored.